

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Fukudome, Kenji  
Esmon, Charles T.

(ii) TITLE OF INVENTION: Cloning and Regulation of an Endothelial  
Cell Protein C/Activated Protein C Receptor

(iii) NUMBER OF SEQUENCES: 6

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Patrea L. Pabst  
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Street  
(C) CITY: Atlanta  
(D) STATE: Georgia  
(E) COUNTRY: US  
(F) ZIP: 30306-3450

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/289,699  
(B) FILING DATE: 12-AUG-1994  
(C) CLASSIFICATION: 530

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pabst, Patrea L.  
(B) REGISTRATION NUMBER: 31,284  
(C) REFERENCE/DOCKET NUMBER: OMRF152

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (404) 873-8794  
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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1302 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..1302

(D) OTHER INFORMATION: /note= "Nucleotides 25 through 738 encode the

Endothelial Cell Protein Receptor of Sequence ID No. 2."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGTCCGGA GCCTCAACTT CAGGATGTTG ACAACATTGC TGCCGATACT GCTGCTGTCT 60  
GGCTGGGCCT TTTGTAGCCA AGACGCCTCA GATGGCCTCC AAAGACTTCA TATGCTCCAG 120  
ATCTCCTACT TCCGCGACCC CTATCACGTG TGGTACCAGG GCAACGCGTC GCTGGGGGGA 180  
CACCTAACGC ACGTGCTGGA AGGCCCAGAC ACCAACACCA CGATCATTCA GCTGCAGCCC 240  
TTGCAGGAGC CCGAGAGCTG GCGCGCACG CAGAGTGGCC TGCAGTCCTA CCTGCTCCAG 300  
TTCCACGGCC TCGTGCGCCT GGTGCACCAG GAGCGGACCT TGGCCTTTCC TCTGACCATC 360  
CGCTGCTTCC TGGGCTGTGA GCTGCCTCCC GAGGGCTCTA GAGCCCATGT CTTCTTCGAA 420  
GTGGCTGTGA ATGGGAGCTC CTTTGTGAGT TTCCGGCCGG AGAGAGCCTT GTGGCAGGCA 480  
GACACCCAGG TCACCTCCGG AGTGGTCACC TTCACCCTGC AGCAGCTCAA TGCCTACAAC 540  
CGCACTCGGT ATGAACTGCG GGAATTCCTG GAGGACACCT GTGTGCAGTA TGTGCAGAAA 600  
CATATTTCCG CGGAAAACAC GAAAGGGAGC CAAACAAGCC GCTCCTACAC TTCGCTGGTC 660  
CTGGGCGTCC TGGTGGGCGG TTTCATCATT GCTGGTGTGG CTGTAGGCAT CTTCTGTGTC 720  
ACAGGTGGAC GCGGATGTTA ATTACTCTCC AGCCCCGTCA GAAGGGGCTG GATTGATGGA 780  
GGCTGGCAAG GGAAAGTTTC AGCTCACTGT GAAGCCAGAC TCCCCAACTG AAACACCAGA 840  
AGGTTTGGAG TGACAGCTCC TTTCTTCTCC CACATCTGCC CACTGAAGAT TTGAGGGAGG 900  
GGAGATGGAG AGGAGAGGTG GACAAAGTAC TTGGTTTGCT AAGAACCTAA GAACGTGTAT 960  
GCTTTGCTGA ATTAGTCTGA TAAGTGAATG TTTATCTATC TTTGTGAAA ACAGATAATG 1020  
GAGTTGGGGC AGGAAGCCTA TGCGCCATCC TCCAAAGACA GACAGAATCA CCTGAGGCGT 1080  
TCAAAAGATA TAACCAATA AACAGTCAT CCACAATCAA AATACAACAT TCAATACTTC 1140  
CAGGTGTGTC AGACTTGGGA TGGGACGCTG ATATAATAGG GTAGAAAGAA GTAACACGAA 1200  
GAAGTGGTGG AAATGTAAAA TCCAAGTCAT ATGGCAGTGA TCAATTATTA ATCAATTAAT 1260  
AATATTAATA AATTTCTTAT ATTTAAAAA AAAAAAAAAA AA 1302

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..365

(D) OTHER INFORMATION: /note= "Endothelial Cell Protein Receptor encoded by nucleotides 1 through 1302 of Sequence ID No. 1."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "Amino acids 1-15 represent a putative signal sequence."

(ix) FEATURE:

(A) NAME/KEY: Domain

(B) LOCATION: 211..236

(D) OTHER INFORMATION: /note= "Amino acids 211-236 represent a putative transmembrane domain."

(ix) FEATURE:

(A) NAME/KEY: Active-site

(B) LOCATION: 47..174

(D) OTHER INFORMATION: /note= "Amino acids 47-49, 64-66, 136-138 and 172-174 represent potential N-glycosylation sites."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17..186

(D) OTHER INFORMATION: /note= "Amino acids 17, 114, 118 and 186 represent extracellular cysteine residues."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Thr Thr Leu Leu Pro Ile Leu Leu Leu Ser Gly Trp Ala Phe  
1 5 10 15

Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln Arg Leu His Met Leu Gln  
20 25 30

Ile Ser Tyr Phe Arg Asp Pro Tyr His Val Trp Tyr Gln Gly Asn Ala  
35 40 45

Ser Leu Gly Gly His Leu Thr His Val Leu Glu Gly Pro Asp Thr Asn  
50 55 60

Thr Thr Ile Ile Gln Leu Gln Pro Leu Gln Glu Pro Glu Ser Trp Ala  
65 70 75 80

Arg Thr Gln Ser Gly Leu Gln Ser Tyr Leu Leu Gln Phe His Gly Leu  
85 90 95

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Val Arg Leu Val His Gln Glu Arg Thr Leu Ala Phe Pro Leu Thr Ile
      100                      105                      110

Arg Cys Phe Leu Gly Cys Glu Leu Pro Pro Glu Gly Ser Arg Ala His
      115                      120                      125

Val Phe Phe Glu Val Ala Val Asn Gly Ser Ser Phe Val Ser Phe Arg
      130                      135                      140

Pro Glu Arg Ala Leu Trp Gln Ala Asp Thr Gln Val Thr Ser Gly Val
      145                      150                      155                      160

Val Thr Phe Thr Leu Gln Gln Leu Asn Ala Tyr Asn Arg Thr Arg Tyr
      165                      170                      175

Glu Leu Arg Glu Phe Leu Glu Asp Thr Cys Val Gln Tyr Val Gln Lys
      180                      185                      190

His Ile Ser Ala Glu Asn Thr Lys Gly Ser Gln Thr Ser Arg Ser Tyr
      195                      200                      205

Thr Ser Leu Val Leu Gly Val Leu Val Gly Gly Phe Ile Ile Ala Gly
      210                      215                      220

Val Ala Val Gly Ile Phe Leu Cys Thr Gly Gly Arg Arg Cys
      225                      230                      235

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Leu Thr Lys Phe Leu Leu Leu Leu Leu Leu Leu Pro Gly Cys
1           5           10           15

Ala Phe Val Thr Pro Met Ala Pro Lys Ala Ala Tyr Ala Pro Asp Leu
      20           25           30

Leu Phe Pro Arg Pro Pro Ser Cys Glu Ala Ser Gly Gln Arg Ser Leu
      35           40           45

Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val Thr
      50           55           60

Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg Thr
      65           70           75           80

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Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val Lys  
                     85                    90                    95  
 Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr Val  
                     100                    105                    110  
 Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Glu Glu Gly Ser  
                     115                    120                    125  
 Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe Val  
                     130                    135                    140  
 Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu Pro  
                     145                    150                    155                    160  
 Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn Arg  
                     165                    170                    175  
 Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu Phe  
                     180                    185                    190  
 Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr Gly  
                     195                    200                    205  
 Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe Ile  
                     210                    215                    220  
 Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg Gly  
                     225                    230                    235                    240  
 Leu Leu Ile Ile

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp  
 1                    5                    10                    15  
 Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln  
                     20                    25                    30  
 Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala  
                     35                    40                    45  
 Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr

50	55	60
Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln		
65	70	75 80
Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr		
	85	90 95
Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu		
	100	105 110
Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser		
	115	120 125
Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe		
	130	135 140
Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn		
	145	150 155 160
Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val		
	165	170 175
Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu		
	180	185 190
Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp		
	195	200 205
Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Val Cys		
	210	215 220
His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg		
	225	230 235 240
Gly Glu Gln Glu Gln Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn		
	245	250 255
Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly		
	260	265 270
Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly		
	275	280 285
Gln Asp Ile Val Leu Tyr Trp Gly Gly Ser Tyr Thr Ser Met Gly Leu		
	290	295 300
Ile Ala Leu Ala Val Leu Ala Cys Leu Leu Phe Leu Leu Ile Val Gly		
	305	310 315 320
Phe Thr Ser Arg Phe Lys Arg Gln Thr Ser Tyr Gln Gly Val Leu		
	325	330 335

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Arg	Tyr	Leu	Pro	Cys	Leu	Leu	Leu	Trp	Ala	Phe	Leu	Gln	Val	Trp	
1				5					10					15		
Gly	Gln	Ser	Glu	Val	Gln	Gln	Lys	Asn	Tyr	Thr	Phe	Arg	Cys	Leu	Gln	
			20					25					30			
Thr	Ser	Ser	Phe	Ala	Asn	Ile	Ser	Trp	Ser	Arg	Thr	Asp	Ser	Leu	Ile	
		35					40					45				
Leu	Leu	Gly	Asp	Leu	Gln	Thr	His	Arg	Trp	Ser	Asn	Asp	Ser	Ala	Thr	
	50					55					60					
Ile	Ser	Phe	Thr	Lys	Pro	Trp	Ser	Gln	Gly	Lys	Leu	Ser	Asn	Gln	Gln	
65					70					75					80	
Trp	Glu	Lys	Leu	Gln	His	Met	Phe	Gln	Val	Tyr	Arg	Val	Ser	Phe	Thr	
			85						90					95		
Arg	Asp	Ile	Gln	Glu	Leu	Val	Lys	Met	Met	Ser	Pro	Lys	Glu	Asp	Tyr	
			100					105					110			
Pro	Ile	Glu	Ile	Gln	Leu	Ser	Thr	Gly	Cys	Glu	Met	Tyr	Pro	Gly	Asn	
		115					120					125				
Ala	Ser	Glu	Ser	Phe	Phe	His	Val	Ala	Phe	Gln	Gly	Lys	Tyr	Ala	Val	
	130					135					140					
Arg	Phe	Arg	Gly	Thr	Ser	Trp	Gln	Arg	Val	Leu	Gly	Ala	Pro	Ser	Trp	
145					150					155					160	
Leu	Asp	Leu	Pro	Ile	Lys	Val	Leu	Asn	Ala	Asp	Gln	Gly	Thr	Ser	Ala	
			165					170					175			
Thr	Val	Gln	Thr	Leu	Leu	Asn	Asp	Thr	Trp	Pro	Gln	Phe	Ala	Arg	Gly	
		180						185					190			
Leu	Leu	Glu	Ala	Gly	Lys	Ser	Asp	Leu	Glu	Lys	Gln	Glu	Lys	Pro	Val	
	195						200					205				
Ala	Trp	Leu	Ser	Ser	Val	Pro	Ser	Ser	Ala	His	Gly	His	Leu	Gln	Leu	
	210					215					220					
Val	Cys	His	Val	Ser	Gly	Phe	Tyr	Pro	Lys	Pro	Val	Trp	Val	Met	Trp	
225					230					235				240		
Met	Arg	Gly	Asp	Gln	Glu	Gln	Gln	Gly	Thr	His	Arg	Gly	Asp	Phe	Leu	

245	250	255
Pro Asn Ala Asp Glu Thr Trp Tyr Leu Gln Ala Thr Leu Asp Val Glu		
260	265	270
Ala Gly Glu Glu Ala Gly Leu Ala Cys Arg Val Lys His Ser Ser Leu		
275	280	285
Gly Gly Gln Asp Ile Ile Leu Tyr Trp Asp Ala Arg Gln Ala Pro Val		
290	295	300
Gly Leu Ile Val Phe Ile Val Leu Ile Met Leu Val Val Val Gly Ala		
305	310	315
Val Val Tyr Tyr Ile Trp Arg Arg Arg Ser Ala Tyr Gln Asp Ile Arg		
325	330	335

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Thr Lys Phe Leu Pro Leu Leu Leu Leu Leu Pro Gly Cys		
1	5	10
Ala Leu Cys Asn Ser Asp Gly Ser Gln Ser Leu His Met Leu Gln Ile		
20	25	30
Ser Tyr Phe Gln Asp His His His Val Arg His Gln Gly Asn Ala Ser		
35	40	45
Leu Gly Lys Leu Leu Thr His Thr Leu Glu Gly Pro Ser Gln Asn Val		
50	55	60
Thr Ile Leu Gln Leu Gln Pro Trp Gln Asp Pro Glu Ser Trp Glu Arg		
65	70	75
Thr Glu Ser Gly Leu Gln Ile Tyr Leu Thr Gln Phe Glu Ser Leu Val		
85	90	95
Lys Leu Val Tyr Arg Glu Arg Lys Glu Asn Val Phe Phe Pro Leu Thr		
100	105	110
Val Ser Cys Ser Leu Gly Cys Glu Leu Pro Glu Glu Glu Glu Gly		
115	120	125
Ser Glu Pro His Val Phe Phe Asp Val Ala Val Asn Gly Ser Ala Phe		



130 135 140

Val Ser Phe Arg Pro Lys Thr Ala Val Trp Val Ser Gly Ser Gln Glu  
145 150 155 160

Pro Ser Lys Ala Ala Asn Phe Thr Leu Lys Gln Leu Asn Ala Tyr Asn  
165 170 175

Arg Thr Arg Tyr Glu Leu Gln Glu Phe Leu Gln Asp Thr Cys Val Glu  
180 185 190

Phe Leu Glu Asn His Ile Thr Thr Gln Asn Met Lys Gly Ser Gln Thr  
195 200 205

Gly Arg Ser Tyr Thr Ser Leu Val Leu Gly Ile Leu Met Gly Cys Phe  
210 215 220

Ile Ile Ala Gly Val Ala Val Gly Ile Phe Met Cys Thr Ser Gly Arg  
225 230 235 240

Arg Cys

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C!  
Cont